

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

Ciossek, Thomas
Ullrich, Axel
Millauer, Birgit

(ii) TITLE OF INVENTION:

METHODS FOR DIAGNOSIS
AND TREATMENT OF MDK1
SIGNAL TRANSDUCTION
DISORDERS

(iii) NUMBER OF SEQUENCES:

12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Lyon & Lyon
(B) STREET: 633 West Fifth Street
Suite 4700
(C) CITY: Los Angeles
(D) STATE: California
(E) COUNTRY: U.S.A.
(F) ZIP: 90071-2066

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: Word Perfect 5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/368,776
(B) FILING DATE: January 3, 1995
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

Prior applications total,
including application
described below:

none

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(1) GENERAL INFORMATION:

(i) APPLICANT: Ciossek, Thomas
Ullrich, Axel
Millauer, Birgit

T, 1040
(ii) TITLE OF INVENTION: METHODS FOR DIAGNOSIS
AND TREATMENT OF MDK1
SIGNAL TRANSDUCTION
DISORDERS

(iii) NUMBER OF SEQUENCES: 12

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(B) STREET: 633 West Fifth Street
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(A) APPLICATION NUMBER: 08/368,776
(B) FILING DATE: January 3, 1995
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

Prior applications total,
including application
described below: none

(A) APPLICATION NUMBER:
 (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Warburg, Richard J.
 (B) REGISTRATION NUMBER: 32,327
 (C) REFERENCE/DOCKET NUMBER: 208/007

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (213) 489-1600
 (B) TELEFAX: (213) 955-0440
 (C) TELEX: 67-3510

(2) INFORMATION FOR SEQUENCE ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AAGCGGCCGG	TCTGCAGTCG	GAGACTTGCA	GGCAGCAAAC	ACGGTGCAGAA	50
CGAACCGGAG	GGGGGAGAGA	GAAATCAAAC	AGCTAAGCGT	GGAGCAGACG	100
GCCTGGGACC	CAGAAGGGGA	TCGATGCGAG	GAGCGCAATA	ATAACAACAA	150
TAATAACCCA	CTTCGGAGCA	AACAGCATCT	AAAGAGCTGC	GACCCAACTG	200
CAGCCTAAAAA	AAATCAAACC	TGCTCATGCA	CCATGGTTGT	TCAAACCTCGG	250
TTCCCTTCGT	GGATTATTTT	GTGTTACATC	TGGCTGCTTG	GCTTGACACA	300
CACGGGGAG	GCGCAGGCTG	CGAAGGAAGT	ACTATTACTG	GACTCGAAAG	350
CACAACAAAC	AGAATTGGAA	TGGATTCCT	CTCCACCCAG	TGGGTGGGAA	400
GAAATTAGTG	GTGGATGAA	GAACACTAC	CCGATAAGAA	CATACCAGGT	450
GTGCCAGGTC	ATGGAGCCA	ACCAGAACAA	CTGGCTGCGG	ACTAACTGGA	500
TTTCTAAAGG	CAACGCACAA	AGGATTGAA	TAGAATTGAA	ATTCACCTTG	550
AGGGATTGTA	ATAGTCTTCC	CGGAGTCCTG	GGAACTTGCA	AGGAAACGTT	600

TAATTTGTAC TATTATGAAA CAGACTACGA CACCGGCAGG AATATACGAG	650
AAAACCTTTA TGTTAAAATA GACACCATTG CTGCAGATGA AAGTTTCACA	700
CAAGGTGACC TTGGTGAAAG AAAGATGAAG CTGAACACTG AGGTGAGAGA	750
GATTGGACCT TTGTCCAAAAG AGGGATTCTA TCTTGCTTT CAGGATGTAG	800
GGGCTTGCAT AGCATTGGTT TCTGTCAAAG TGTACTACAA GAAGTGCTGG	850
ACCATTGTTG AGAACTTAGC TGTCTTCCA GATACAGTGA CTGGTTCGGA	900
ATTTCCCTCC TTAGTCGAGG TCCGTGGAC ATGTGTCAGC AGTGCCGAGG	950
AAGAGGCAGA AAATTCCCCC AGAATGCATT GCAGTGCAGA AGGAGAGTGG	1000
CTAGTACCCA TTGGAAAATG CATCTGAAA GCAGGCTATC AGCAAAAGG	1050
GGACACTTGC GAACCTGTG GCCGCAGGTT CTACAAATCT TCCTCTCAGG	1100
ATCTCCAGTG TTCTCGTTGT CCAACCCACA GCTTCTCTGA CCGAGAAGGA	1150
TCATCCAGGT GTGAATGTGA AGATGGGTAC TACAGAGCTC CTTCTGATCC	1200
ACCATACGTT GCATGCACGA GGCCTCCCTC TGCACCACAG AACCTTATTT	1250
TCAATATCAA TCAAACGACT GTAAGTTGG AATGGAGTCC TCCGGCTGAC	1300
AACGGGGGAA GAAACGATGT CACCTACAGA ATACTGTGTA AGCGGTGCAG	1350
TTGGGAACAG GGAGAAATGTG TGCCATGCGG AAGTAACATT GGATACATGC	1400
CCCAGCAGAC GGGATTAGAG GATAACTATG TCACTGTCAT GGACCTACTT	1450
GCCCATGCAA ATTACACTTT CGAAGTTGAA GCTGTAAATG GAGTTTCAGG	1500
CTTAAGCAGA TCCCAGAGGC TCTTCGCTGC TGTTAGCATC ACCACCGGTC	1550
AAGCAGCTCC CTCGCAAGTG AGTGGAGTCA TGAAGGAGCG AGTACTGCAG	1600
CGGAGTGTGC AGCTTCCCTG GCAGGAGCCG GAGCATCCCA ATGGAGTCAT	1650
CACGGAATAT GAAATCAAGT ATTATGAGAA AGATCAACGG GAAAGGACGT	1700
ACTCAACACT CAAAACCAAG TCCACCTCCG CCTCCATTAA TAATCTGAAA	1750
CCGGGAACAG TGTACGTCTT TCAGATCCGG GCGGTCACTG CTGCCGGTTA	1800
TGGAAACTAC AGCCCTAGGC TTGATGTTGC CACACTTGAG GAAGCTTCAG	1850
GTAAAATGTT TGAAGCGACA GCAGTCTCCA GTGAACAGAA TCCTGTCATC	1900
ATAATTGCTG TAGTGGCTGT AGCAGGGACC ATCATCTTGG TGTTCATGGT	1950
GTTCGGCTTC ATCATTGGAA GAAGGCAGTG TGGTTATAGC AAGGCTGACC	2000

AAGAAGGGGA	TGAAGAACTC	TACTTCATT	TTAAATTC	AGGCACCAAA	2050
ACCTACATTG	ACCCGTAAAC	CTATGAGGAC	CCAAATAGAG	CTGTCCATCA	2100
ATTGCCAAG	GAGCTAGATG	CCTCCTGTAT	TAAAATTGAG	CGTGTGATTG	2150
GTGCAGGAGA	ATTTGGAGAA	GTTCAGTG	GTCGTTGAA	ACTTCCGGGC	2200
CAGAGAGATG	TTGCAGTGGC	CATAAAAACC	CTGAAAGTTG	GTTACACAGA	2250
AAAGCAAAGG	AGGGACTTTT	TATGCGAAGC	AAGCATCATG	GGGCAATTG	2300
ACCACCCAAA	TGTCGTCCAT	TTGGAAGGGG	TTGTTACAAG	AGGGAAGCCT	2350
GTCATGATTG	TGATAGAGTT	CATGGAGAAT	GGAGCCCTGG	ATGCATTCT	2400
CAGGAAACAC	GATGGGCAGT	TTACAGTCAT	TCAGTTGGTA	GGAATGTTGA	2450
GAGGTATTGC	CGCTGGGATG	CGATACTTGG	CTGATATGGG	ATACGTTCAC	2500
AGGGACCTTG	CAGCGCGCAA	CATCCTTGT	AACAGCAATC	TTGTTGTAA	2550
AGTGTCAAGAT	TTTGGCCTTT	CCCGGTTAT	AGAGGATGAT	CCCGAAGCTG	2600
TCTACACCAC	GAUTGGTGGA	AAAATTCCAG	TAAGGTGGAC	TGCACCGGAA	2650
GCCATTCAAT	ACCGGAAGTT	CACCTCAGCC	AGCGATGTGT	GGAGCTATGG	2700
GATTGTCATG	TGGGAAGTGA	TGTCTTATGG	AGAAAGACCT	TACTGGGACA	2750
TGTCAAATCA	AGATGTCATT	AAAGCGATAG	AAGAAGGTTA	TCGTTGCCG	2800
GCGCCCATGG	ATTGCCAGC	TGGTCTTCAC	CAGCTAATGC	TGGATTGTTG	2850
GCAGAAAGAT	CGGGCGGAAA	GGCAAAGTT	TGAGCAGATA	GTCGGAATTC	2900
TAGACAAAAT	GATTGAAAC	CCAAGTAGTC	TGAAAACACC	CCTGGAACT	2950
TGTAGTAGAC	CCTTAAGCCC	TCTTCTGGAC	CAGAGCACTC	CTGACTTCAC	3000
TGCCTTCTGT	TCAGTTGGAG	AATGGTTGCA	AGCTATTAAA	ATGGAAAGGT	3050
ATAAGGACAA	CTTCACAGCA	GCAGGTTACA	ACTCACTCGA	GTCAGTGGCC	3100
AGGATGACTA	TCGATGATGT	GATGAGTTA	GGGATCACAC	TGGTTGCCA	3150
TCAAAAGAAG	ATCATGAGCA	GCATCCAGAC	TATGCGGGCA	CAAATGTTGC	3200
ATTACACGG	AACAGGCATC	CAAGTGTGAC	ACATCGGCCT	CCCTCAGATG	3250
AGGCTTAAGA	CTGCAGGAGA	ACAGTTCTGG	CCTTCAGTAT	ACGCATAGAA	3300
TGCTGCTAGA	AGACAGTTGA	TATACTGGGT	CCTTCCTACA	AGAAAGAGAA	3350
GATTTAGAA	GCACCTCCAG	ACTTGAACTC	CTAAGTGCCA	CCAGAAATATA	3400

CAAAAAGGGA	ATTTAGGATC	CAACCACTGGT	GGCCAGGAAC	ACAGCAGAGA	3450
CAATAAACAA	AGTACTACCT	GAAAAACATC	CCAACACCTT	GAGCTCTCGA	3500
ACCTCCTTTT	TATCTTATAG	ACTTTTAAA	AATGTACATA	AAGAATTAA	3550
GAAAGAATAT	ATTTGTCAAA	AAAAAATCAT	GATCTTATTG	TTAAAATCAA	3600
TGAAATATTT	TCCTTAAAAT	ATGTGATTTC	AGACTATTCT	TTTCCAGAAC	3650
CATCTGTGTT	TATTCTGCTT	AAGGACTTTG	TTTTAGAAAG	TTATTTGTAG	3700
CTTGGACCT	TTTTAGTGTT	AAATTTATGA	CACGTTACTA	CACTGGAAC	3750
CTTGAAGAC	TCTCAAACCT	AAAGGAAAGC	AAAACATACGC	ACATAGTCGA	3800
GGATGGACTT	TGTCCTTCAT	GGCTTGGTA	TCCTGGCTGT	GTCATTTGT	3850
TAAACCAGTG	ATGTTTCAT	ATTGTTGCT	GATTGGCAGG	TAGTTCAAAA	3900
TTGCAAGTTG	CCAAGAGCTC	TGATATTTT	TAACAGGATT	TTTTTTCTT	3950
TGTAAAATC	AGATAACATA	CTAACTTTTC	AATGAAAAAA	AAAAAAAAG	4000
AAGCAATAAT	GATCCATAAA	TACTATAAGG	CACTTTAAC	AGATTGTTA	4050
TAGAGTGATT	TACTAGGCAG	AATTAAATAA	AAAAAAAAGA	GAGATGTCAA	4100
ATTTAGGTT	TATGTGTATA	TGATAAAAGG	CTGAGCTTCG	TCTGAAGATG	4150
CTGGTGAAAG	CAAGACTGGA	AGCGAAGCTC	TCCAGCTTG	GCTAACCCAA	4200
TCCGAGCACA	TCAAGAGCTT	CAGTCTGTTG	ACAGTAAGAA	ATTTAGGAAC	4250
ATAGTTGACC	TATATTTGT	ATTCTTCTT	GTTGAATGCA	GTCCAAATAC	4300
AAAA					4304

(2) INFORMATION FOR SEQUENCE ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 998 amino acids
- (B) TYPE: amino acid
- (C) STRANDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Val Val Gln Thr Arg Phe Pro Ser Trp Ile Ile Leu Cys Tyr Ile
 1 5 10 15

Trp Leu Leu Gly Phe Ala His Thr Gly Glu Ala Gln Ala Ala Lys Glu
 20 25 30

Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile
 35 40 45

Ser Ser Pro Pro Ser Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn
 50 55 60

Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn
 65 70 75 80

Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln
 85 90 95

Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu
 100 105 110

Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr
 115 120 125

Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val
 130 135 140

Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu
 145 150 155 160

Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro
 165 170 175

Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys
 180 185 190

Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Thr Ile
 195 200 205

Val Glu Asn Leu Ala Val Phe Pro Asp Thr Val Thr Gly Ser Glu Phe
 210 215 220

Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu
 225 230 235 240

Glu Ala Glu Asn Ser Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp
 245 250 255

Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys
 260 265 270

Gly Asp Thr Cys Glu Pro Cys Gly Arg Arg Phe Tyr Lys Ser Ser Ser
 275 280 285

Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Arg
 290 295 300

Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro
 305 310 315 320

Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln
 325 330 335

Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser
 340 345 350

Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu
 355 360 365

Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser
 370 375 380

Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val
 385 390 395 400

Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu
 405 410 415

Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala
 420 425 430

Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly
 435 440 445

Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Gln Leu Ser Trp Gln
 450 455 460

Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr
 465 470 475 480

Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Leu Lys Thr Lys
 485 490 495

Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val
 500 505 510

Phe Gln Ile Arg Ala Val Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro
 515 520 525

Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Ser Gly Lys Met Phe Glu
 530 535 540

Ala Thr Ala Val Ser Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val
 545 550 555 560

Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe
 565 570 575

Ile Ile Gly Arg Arg His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly
 580 585 590

Asp Glu Glu Leu Tyr Phe His Phe Lys Phe Pro Gly Thr Lys Thr Tyr
 595 600 605

Ile Asp Pro Glu Thr Tyr Glu Asp Pro Asn Arg Ala Val His Gln Phe
 610 615 620

Ala Lys Glu Leu Asp Ala Ser Cys Ile Lys Ile Glu Arg Val Ile Gly
 625 630 635 640

Ala Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Leu Pro Gly
 645 650 655

Gln Arg Asp Val Ala Val Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr
 660 665 670

Glu Lys Gln Arg Arg Asp Phe Leu Cys Glu Ala Ser Ile Met Gly Gln
 675 680 685

Phe Asp His Pro Asn Val Val His Leu Glu Gly Val Val Thr Arg Gly
 690 695 700

Lys Pro Val Met Ile Val Ile Glu Phe Met Glu Asn Gly Ala Leu Asp
 705 710 715 720

Ala Phe Leu Arg Lys His Asp Gly Gln Phe Thr Val Ile Gln Leu Val
 725 730 735

Gly Met Leu Arg Gly Ile Ala Ala Gly Met Arg Tyr Leu Ala Asp Met
 740 745 750

Gly Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser
 755 760 765

Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Ile Glu
 770 775 780

Asp Asp Pro Glu Ala Val Tyr Thr Thr Thr Gly Gly Lys Ile Pro Val
 785 790 795 800

Arg Trp Thr Ala Pro Glu Ala Ile Gln Tyr Arg Lys Phe Thr Ser Ala
 805 810 815

Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr
 820 825 830

Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala
 835 840 845

Ile Glu Glu Gly Tyr Arg Leu Pro Ala Pro Met Asp Cys Pro Ala Gly
 850 855 860
 Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Asp Arg Ala Glu Arg
 865 870 875 880
 Pro Lys Phe Glu Gln Ile Val Gly Ile Leu Asp Lys Met Ile Arg Asn
 885 890 895
 Pro Ser Ser Leu Lys Thr Pro Leu Gly Thr Cys Ser Arg Pro Leu Ser
 900 905 910
 Pro Leu Leu Asp Gln Ser Thr Pro Asp Phe Thr Ala Phe Cys Ser Val
 915 920 925
 Gly Glu Trp Leu Gln Ala Ile Lys Met Glu Arg Tyr Lys Asp Asn Phe
 930 935 940
 Thr Ala Ala Gly Tyr Asn Ser Leu Glu Ser Val Ala Arg Met Thr Ile
 945 950 955 960
 Asp Asp Val Met Ser Leu Gly Ile Thr Leu Val Gly His Gln Lys Lys
 965 970 975
 Ile Met Ser Ser Ile Gln Thr Met Arg Ala Gln Met Leu His Leu His
 980 985 990
 Gly Thr Gly Ile Gln Val
 995

(2) INFORMATION FOR SEQUENCE ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 amino acids
- (B) TYPE: amino acid
- (C) STRANDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Val Val Gln Thr Arg Phe Pro Ser Trp Ile Ile Leu Cys Tyr Ile
 1 5 10 15
 Trp Leu Leu Gly Phe Ala His Thr Gly Glu Ala Gln Ala Ala Lys Glu
 20 25 30
 Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile
 35 40 45

Ser Ser Pro Pro Ser Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn
 50 55 60

Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn
 65 70 75 80

Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln
 85 90 95

Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu
 100 105 110

Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr
 115 120 125

Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val
 130 135 140

Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu
 145 150 155 160

Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro
 165 170 175

Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys
 180 185 190

Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Thr Ile
 195 200 205

Val Glu Asn Leu Ala Val Phe Pro Asp Thr Val Thr Gly Ser Glu Phe
 210 215 220

Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu
 225 230 235 240

Glu Ala Glu Asn Ser Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp
 245 250 255

Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys
 260 265 270

Gly Asp Thr Cys Glu Pro Cys Gly Arg Arg Phe Tyr Lys Ser Ser Ser
 275 280 285

Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Arg
 290 295 300

Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro
 305 310 315 320

Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln
 325 330 335

Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser
 340 345 350

Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu
 355 360 365

Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser
 370 375 380

Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val
 385 390 395 400

Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu
 405 410 415

Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala
 420 425 430

Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly
 435 440 445

Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Gln Leu Ser Trp Gln
 450 455 460

Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr
 465 470 475 480

Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Leu Lys Thr Lys
 485 490 495

Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val
 500 505 510

Phe Gln Ile Arg Ala Val Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro
 515 520 525

Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Ser Gly Lys Met Phe Glu
 530 535 540

Ala Thr Ala Val Ser Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val
 545 550 555 560

Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe
 565 570 575

Ile Ile Gly Arg Arg His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly
 580 585 590

Asp Glu Glu Leu Tyr Phe His Ser Leu Val Thr Asn Glu His Leu Ser
 595 600 605

Val Leu
 610

(2) INFORMATION FOR SEQUENCE ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2901 base pairs
 (B) TYPE: nucleic acid
 (C) STRANNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AAGCGGCCGG	TCTGCAGTCG	GAGACTTGCA	GGCAGCAAAC	ACGGTGCAGA	50
CGAACCGGAG	GGGGGAGAGA	GAAATCAAAC	AGCTAAGCGT	GGAGCAGACG	100
GCCTGGGACC	CAGAAGGGGA	TCGATGCGAG	GAGCGCAATA	ATAACAACAA	150
TAATAACCCA	CTTCGGAGCA	AACAGCATCT	AAAGAGCTGC	GACCCAACGT	200
CAGCCTAAAAA	AAATCAAACC	TGCTCATGCA	CCATGGTTGT	TCAAACCTCGG	250
TTCCCTTCGT	GGATTATTTT	GTGTTACATC	TGGCTGCTTG	GCTTGACACA	300
CACGGGGGAG	GCGCAGGCTG	CGAAGGAAGT	ACTATTACTG	GACTCGAAAG	350
CACAACAAAC	AGAATTGGAA	TGGATTTCCT	CTCCACCCAG	TGGGTGGGAA	400
GAAATTAGTG	GTGGGATGAA	GAACTACACT	CCGATAAGAA	CATACCAGGT	450
GTGCCAGGTC	ATGGAGCCCA	ACCAGAACAA	CTGGCTGCGG	ACTAACTGGA	500
TTTCTAAAGG	CAACGCACAA	AGGATTTTG	TAGAATTGAA	ATTCACCTTG	550
AGGGATTGTA	ATAGTCTTCC	CGGAGTCCTG	GGAACTTGCA	AGGAAACGTT	600
TAATTTGTAC	TATTATGAAA	CAGACTACGA	CACCGGCAGG	AATATACGAG	650
AAAACCTTTA	TGTTAAAATA	GACACCATTG	CTGCAGATGA	AAGTTTCACA	700
CAAGGTGACC	TTGGTGAAAG	AAAGATGAAG	CTGAACACTG	AGGTGAGAGA	750
GATTGGACCT	TTGTCCAAAA	AGGGATTCTA	TCTTGCCITT	CAGGATGTAG	800
GGGCTTGCAT	AGCATTGGTT	TCTGTCAAAG	TGTACTACAA	GAAGTGCTGG	850
ACCATTGTTG	AGAACTTAGC	TGTCTTCCA	GATACAGTGA	CTGGTTGGAA	900
ATTTTCCTCC	TTAGTCGAGG	TCCGTGGGAC	ATGTGTCAGC	AGTGCCGAGG	950
AAGAGGCAGA	AAATTCCCCC	AGAATGCATT	GCAGTGCAGA	AGGAGAGTGG	1000
CTAGTACCCA	TTGGAAAATG	CATCTGCAAA	GCAGGGCTATC	AGCAAAAAGG	1050

GGACACTTGC GAACCTGTG GCCGCAGGTT CTACAAATCT TCCTCTCAGG 1100
 ATCTCCAGTG TTCTCGTTGT CCAACCCACA GCTTCTCTGA CCGAGAAGGA 1150
 TCATCCAGGT GTGAATGTGA AGATGGGTAC TACAGAGCTC CTTCTGATCC 1200
 ACCATACGTT GCATGCACGA GGCCTCCCTC TGCACCACAG AACCTTATTT 1250
 TCAATATCAA TCAAACGACT GTAAGTTGG AATGGAGTCC TCCGGCTGAC 1300
 AACGGGGAA GAAACGATGT CACCTACAGA ATACTGTGTA AGCGGTGCAG 1350
 TTGGGAACAG GGAGAAATGTG TGCCATGCGG AAGTAACATT GGATACATGC 1400
 CCCAGCAGAC GGGATTAGAG GATAACTATG TCACTGTCAT GGACCTACTT 1450
 GCCCATGCAA ATTACACTTT CGAAGTTGAA GCTGTAAATG GAGTTTCGGA 1500
 CTTAAGCAGA TCCCAGAGGC TCTTCGCTGC TGTTAGCATC ACCACCGGTC 1550
 AAGCAGCTCC CTCGCAAGTG AGTGGAGTCA TGAAGGAGCG AGTACTGCAG 1600
 CGGAGTGTGC AGCTTCCTG GCAGGAGCCG GAGCATCCCA ATGGAGTCAT 1650
 CACGGAATAT GAAATCAAGT ATTATGAGAA AGATCAACGG GAAAGGACGT 1700
 ACTCAACACT CAAAACCAAG TCCACCTCCG CCTCCATTAA TAATCTGAAA 1750
 CCGGGAACAG TGTACGTCTT TCAGATCCGG GCGGTCACTG CTGCCGGTTA 1800
 TGGAAACTAC AGCCCTAGGC TTGATGTTGC CACACTTGAG GAAGCTTCAG 1850
 GTAAAATGTT TGAAGCGACA GCAGTCTCCA GTGAACAGAA TCCTGTCATC 1900
 ATAATTGCTG TAGTGGCTGT AGCAGGGACC ATCATCTTGG TGTTCATGGT 1950
 GTTCGGCTTC ATCATTGGAA GAAGGCAGTG TGGTTATAGC AAGGCTGACC 2000
 AAGAAGGGGA TGAAGAACTC TACTTCATT CTTTAGTAAC AAATGAGCAC 2050
 CTGTCAGTTT TATAAACCGC AACAAATACT GTTTAAGACA ATCAATTTG 2100
 GATAAACAAAT CAACTACAGC AGAATAAAATC AAGATTTTA AGTCCCATT 2150
 TCCCTTATAC ATTCTGCTTA TTTTGTGTT ATATGTTAT TTTTAAACT 2200
 CTGATCTTGA TTGAATGTGA TACCATAAGC ACAGTTAGGC TGCAGTGTAA 2250
 ATATATAAAAG ACATTGTTCT GAGAGCAGTA CGATTTCATG GAAAGATTGT 2300
 TTGGTGGCTT TGTTAAAATT AATAAAGAAT TTTTAAGGAT ATAGTGTAAAT 2350
 TTTCTTCATT GCATTAATAT AACCAAATAT GCCTACCTAT CTTGTCTTG 2400
 AACCAAATGA ATAGATTGG AATACTTTAT TGTAATTGAA TTTGATATAA 2450

AGTTGACTGA GCATTTATGT GTTACCTGCA TGCTTCTGGG TGCATTGAAA	2500
TATTTTAACT TTTAAAATGA TACTATGTTG TTTCAATTG GACTACCTTT	2550
TGTGAGGCAT ACTGGCTACC TCCTCCTATT AGCTAAGATC TTCCAAAGGCC	2600
TTATAATGAA AAGTTTATAT AAACCATTTC TCTTCAAAT CACTGTCATA	2650
CTTGGTCACG GATCCCAGGA ATATTGTAAA TTTTCTAATT TACTCTGCAC	2700
TTTGTATATC CAGCCTCTAT TACCCCTCAAG GTGAATATAA AACTATGTCT	2750
TTTGAATATT TCTCTTGAT TTTGTGATAG CAGTCCCTCA TATCTTGTAC	2800
TAATTTATG TATATGTCAA CAGTGGTTGG TCTTTAAAAA TAAATCAAAG	2850
AATAAGTAAA AAAAAAAA AAAAAAAA AAAAATAAAA AAAAAAAA	2900
A	2901

(2) INFORMATION FOR SEQUENCE ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	626 amino acids
(B) TYPE:	amino acid
(C) STRANDNESS:	single
(D) TOPOLOGY:	linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Val Val Gln Thr Arg Phe Pro Ser Trp Ile Ile Leu Cys Tyr Ile			
1	5	10	15
Trp Leu Leu Gly Phe Ala His Thr Gly Glu Ala Gln Ala Ala Lys Glu			
20	25	30	
Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile			
35	40	45	
Ser Ser Pro Pro Ser Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn			
50	55	60	
Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn			
65	70	75	80
Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln			
85	90	95	
Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu			
100	105	110	

Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr
 115 120 125

Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val
 130 135 140

Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu
 145 150 155 160

Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro
 165 170 175

Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys
 180 185 190

Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Thr Ile
 195 200 205

Val Glu Asn Leu Ala Val Phe Pro Asp Thr Val Thr Gly Ser Glu Phe
 210 215 220

Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu
 225 230 235 240

Glu Ala Glu Asn Ser Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp
 245 250 255

Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys
 260 265 270

Gly Asp Thr Cys Glu Pro Cys Gly Arg Arg Phe Tyr Lys Ser Ser Ser
 275 280 285

Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Arg
 290 295 300

Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro
 305 310 315 320

Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln
 325 330 335

Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser
 340 345 350

Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu
 355 360 365

Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser
 370 375 380

Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val
 385 390 395 400

Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu
 405 410 415

Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala
 420 425 430

Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly
 435 440 445

Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Gln Leu Ser Trp Gln
 450 455 460

Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr
 465 470 475 480

Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Leu Lys Thr Lys
 485 490 495

Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val
 500 505 510

Phe Gln Ile Arg Ala Val Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro
 515 520 525

Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Ser Gly Lys Met Phe Glu
 530 535 540

Ala Thr Ala Val Ser Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val
 545 550 555 560

Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe
 565 570 575

Ile Ile Gly Arg Arg His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly
 580 585 590

Asp Glu Glu Leu Tyr Phe His Ser Leu Tyr Arg Glu Arg Gly Asp Gly
 595 600 605

Met Glu Lys Thr Gln His Asn Lys Lys Trp Met Ile Ala Ser Cys Ser
 610 615 620

Arg Leu
 625

(2) INFORMATION FOR SEQUENCE ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AAGCGGCCGG	TCTGCAGTCG	GAGACTTGCA	GGCAGCAAAAC	ACGGTGCAGAA	50
CGAACCGGAG	GGGGGAGAGA	GAAATCAAAC	AGCTAAGCGT	GGAGCAGACG	100
GCCTGGGACC	CAGAAGGGGA	TCGATGCGAG	GAGCGCAATA	ATAACAACAA	150
TAATAACCCA	CTTCGGAGCA	AACAGCATCT	AAAGAGCTGC	GACCCAACGT	200
CAGCCTAAAAA	AAATCAAAC	TGCTCATGCA	CCATGGTTGT	TCAAACACTCGG	250
TTCCCTTCGT	GGATTATTTT	GTGTTACATC	TGGCTGCTTG	GCTTTGCACA	300
CACGGGGAG	GCGCAGGCTG	CGAAGGAAGT	ACTATTACTG	GACTCGAAAG	350
CACAACAAAC	AGAATTGGAA	TGGATTTCCT	CTCCACCCAG	TGGGTGGGAA	400
GAAATTAGTG	GTGGATGAA	GAACTACACT	CCGATAAGAA	CATACCAGGT	450
GTGCCAGGTC	ATGGAGCCA	ACCAGAACAA	CTGGCTGCGG	ACTAACTGGA	500
TTTCTAAAGG	CAACGCACAA	AGGATTTTG	TAGAATTGAA	ATTCACCTTG	550
AGGGATTGTA	ATAGTCTTCC	CGGAGTCCTG	GGAACTTGCA	AGGAAACGTT	600
TAATTGTAC	TATTATGAAA	CAGACTACGA	CACCGGCAGG	AATATACGAG	650
AAAACCTTTA	TGTTAAAATA	GACACCATTG	CTGCAGATGA	AAGTTTCACA	700
CAAGGTGACC	TTGGTGAAAG	AAAGATGAAG	CTGAACACTG	AGGTGAGAGA	750
GATTGGACCT	TTGTCCAAAA	AGGGATTCTA	TCTTGCCTTT	CAGGATGTAG	800
GGGCTTGCAT	AGCATTGGTT	TCTGTCAAAG	TGTACTACAA	GAAGTGCTGG	850
ACCATTGTTG	AGAACTTAGC	TGTCTTCCA	GATACTGTA	CTGGTTCGGA	900
ATTTTCTCC	TTAGTCGAGG	TCCGTGGAC	ATGTGTCAGC	AGTGCCGAGG	950
AAGAGGCAGA	AAATTCCCCC	AGAATGCATT	GCAGTGCAGA	AGGAGAGTGG	1000
CTAGTACCCA	TTGGAAAATG	CATCTGCAA	GCAGGCTATC	AGCAAAAAGG	1050
GGACACTTGC	GAACCCGTG	GCCGCAGGTT	CTACAAATCT	TCCTCTCAGG	1100
ATCTCCAGTG	TTCTCGTTGT	CCAACCCACA	GCTTCTCTGA	CCGAGAAGGA	1150
TCATCCAGGT	GTGAATGTGA	AGATGGGTAC	TACAGAGCTC	CTTCTGATCC	1200
ACCATACGTT	GCATGCACGA	GGCCTCCCTC	TGCACCAACAG	AACCTTATTT	1250
TCAATATCAA	TCAAACGACT	GTAAGTTGG	AATGGAGTCC	TCCGGCTGAC	1300

AACGGGGGAA	GAAACGATGT	CACCTACAGA	ATACTGTGTA	AGCGGTGCAG	1350
TTGGGAACAG	GGAGAAATGTG	TGCCATGCGG	AAGTAACATT	GGATACATGC	1400
CCCAGCAGAC	GGGATTAGAG	GATAACTATG	TCACTGTCAT	GGACCTACTT	1450
GCCCATGCAA	ATTACACTTT	CGAAGTTGAA	GCTGTAAATG	GAGTTTCGGA	1500
CTTAAGCAGA	TCCCAGAGGC	TCTTCGCTGC	TGTTAGCATC	ACCACCGGTC	1550
AAGCAGCTCC	CTCGCAAGTG	AGTGGAGTCA	TGAAGGAGCG	AGTACTGCAG	1600
CGGAGTGTGC	AGCTTTCCTG	GCAGGAGCCG	GAGCATCCCA	ATGGAGTCAT	1650
CACGGAATAT	GAAATCAAGT	ATTATGAGAA	AGATCAACGG	GAAAGGACGT	1700
ACTCAACACT	CAAACCAAG	TCCACCTCCG	CCTCCATTAA	TAATCTGAAA	1750
CCGGGAACAG	TGTACGTCTT	TCAGATCCGG	GCGGTCACTG	CTGCCGGTTA	1800
TGGAAACTAC	AGCCCTAGGC	TTGATGTTGC	CACACTTGAG	GAAGCTTCAG	1850
GTAAAATGTT	TGAAGCGACA	GCAGTCTCCA	GTGAACAGAA	TCCTGTCATC	1900
ATAATTGCTG	TAGTGGCTGT	AGCAGGGACC	ATCATCTTGG	TGTTCATGGT	1950
GTTCGGCTTC	ATCATTGGAA	GAAGGCACTG	TGGTTATAGC	AAGGCTGACC	2000
AAGAAGGGGA	TGAAGAACTC	TACTTTCATT	CTCTTTACAG	GGAAAGGGGA	2050
GACGGGATGG	AAAAGACACA	GCACAATAAG	AAAGTGGATGA	TTGCATCGTG	2100
CTCTCGTTG	TAGGTCTCTT	TTCCTAATCA	ACACTATGAT	TTTGAAGTAC	2150
GCGTACACGA	AGCAAACGGG	AAGAGATAAG	GAATTAGCAT	TGTGAACCTG	2200
ACTGTAATCC	TCTCTTCCGG	AAAGAGATGA	GATGCTATTG	CGATGAGAAT	2250
GTACAACTTG	CACCTTGAAA	TCTTTTTGA	TAATTAGTGC	TCAGGGGAGG	2300
GGGGGGGAAG	TAGAGAAAGC	AAA			2323

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Ala Ala Thr Ala Ala Ala
5

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ala Ala Thr Ala Ala Ala
5

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

His Arg Asp Leu Ala Ala
5

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 2 is valine or methionine; Xaa in position 5 is phenylalanine or tyrosine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Asp Xaa Trp Ser Xaa Gly
5

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 993 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Met	Val	Val	Gln	Thr	Arg	Phe	Pro	Ser	Trp	Ile	Ile	Leu	Cys	Tyr	Ile
1										10					15
5															
Trp	Leu	Leu	Gly	Phe	Ala	His	Thr	Gly	Glu	Ala	Gln	Ala	Ala	Lys	Glu
															30
20 25															
Val	Leu	Leu	Leu	Asp	Ser	Lys	Ala	Gln	Gln	Thr	Glu	Leu	Glu	Trp	Ile
															45
35 40															
Ser	Ser	Pro	Pro	Ser	Gly	Trp	Glu	Glu	Ile	Ser	Gly	Leu	Asp	Glu	Asn
															60
50 55															
Tyr	Thr	Pro	Ile	Arg	Thr	Tyr	Gln	Val	Cys	Gln	Val	Met	Glu	Pro	Asn
															80
65 70 75															
Gln	Asn	Asn	Trp	Leu	Arg	Thr	Asn	Trp	Ile	Ser	Lys	Gly	Asn	Ala	Gln
															95
85 90															
Arg	Ile	Phe	Val	Glu	Leu	Lys	Phe	Thr	Leu	Arg	Asp	Cys	Asn	Ser	Leu
															110
100 105															
Pro	Gly	Val	Leu	Gly	Thr	Cys	Lys	Glu	Thr	Phe	Asn	Leu	Tyr	Tyr	Tyr
															125
115 120															
Glu	Thr	Asp	Tyr	Asp	Thr	Gly	Arg	Asn	Ile	Arg	Glu	Asn	Leu	Tyr	Val
															140
130 135															

Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu
 145 150 155 160

Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro
 165 170 175

Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys
 180 185 190

Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Thr Ile
 195 200 205

Val Glu Asn Leu Ala Val Phe Pro Asp Thr Val Thr Gly Ser Glu Phe
 210 215 220

Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu
 225 230 235 240

Glu Ala Glu Asn Ser Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp
 245 250 255

Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys
 260 265 270

Gly Asp Thr Cys Glu Pro Cys Gly Arg Arg Phe Tyr Lys Ser Ser Ser
 275 280 285

Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Arg
 290 295 300

Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro
 305 310 315 320

Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln
 325 330 335

Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser
 340 345 350

Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu
 355 360 365

Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser
 370 375 380

Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val
 385 390 395 400

Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu
 405 410 415

Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala
 420 425 430

Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly
 435 440 445

Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Gln Leu Ser Trp Gln
 450 455 460

Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr
 465 470 475 480

Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Leu Lys Thr Lys
 485 490 495

Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val
 500 505 510

Phe Gln Ile Arg Ala Val Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro
 515 520 525

Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Ser Ala Thr Ala Val Ser
 530 535 540

Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val Val Ala Val Ala Gly
 545 550 555 560

Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe Ile Ile Gly Arg Arg
 565 570 575

His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly Asp Glu Glu Leu Tyr
 580 585 590

Phe His Phe Lys Phe Pro Gly Thr Lys Thr Tyr Ile Asp Pro Glu Thr
 595 600 605

Tyr Glu Asp Pro Asn Arg Ala Val His Gln Phe Ala Lys Glu Leu Asp
 610 615 620

Ala Ser Cys Ile Lys Ile Glu Arg Val Ile Gly Ala Gly Glu Phe Gly
 625 630 635 640

Glu Val Cys Ser Gly Arg Leu Lys Leu Pro Gly Gln Arg Asp Val Ala
 645 650 655

Val Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr Glu Lys Gln Arg Arg
 660 665 670

Asp Phe Leu Cys Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro Asn
 675 680 685

Val Val His Leu Glu Gly Val Val Thr Arg Gly Lys Pro Val Met Ile
 690 695 700

Val Ile Glu Phe Met Glu Asn Gly Ala Leu Asp Ala Phe Leu Arg Lys
 705 710 715 720

His Asp Gly Gln Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg Gly
 725 730 735

Ile Ala Ala Gly Met Arg Tyr Leu Ala Asp Met Gly Tyr Val His Arg
 740 745 750

Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys
 755 760 765

Val Ser Asp Phe Gly Leu Ser Arg Val Ile Glu Asp Asp Pro Glu Ala
 770 775 780

Val Tyr Thr Thr Thr Gly Gly Lys Ile Pro Val Arg Trp Thr Ala Pro
 785 790 795 800

Glu Ala Ile Gln Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser
 805 810 815

Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr Gly Glu Arg Pro Tyr
 820 825 830

Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala Ile Glu Glu Gly Tyr
 835 840 845

Arg Leu Pro Ala Pro Met Asp Cys Pro Ala Gly Leu His Gln Leu Met
 850 855 860

Leu Asp Cys Trp Gln Lys Asp Arg Ala Glu Arg Pro Lys Phe Glu Gln
 865 870 875 880

Ile Val Gly Ile Leu Asp Lys Met Ile Arg Asn Pro Ser Ser Leu Lys
 885 890 895

Thr Pro Leu Gly Thr Cys Ser Arg Pro Leu Ser Pro Leu Leu Asp Gln
 900 905 910

Ser Thr Pro Asp Phe Thr Ala Phe Cys Ser Val Gly Glu Trp Leu Gln
 915 920 925

Ala Ile Lys Met Glu Arg Tyr Lys Asp Asn Phe Thr Ala Ala Gly Tyr
 930 935 940

Asn Ser Leu Glu Ser Val Ala Arg Met Thr Ile Asp Asp Val Met Ser
 945 950 955 960

Leu Gly Ile Thr Leu Val Gly His Gln Lys Lys Ile Met Ser Ser Ile
 965 970 975

Gln Thr Met Arg Ala Gln Met Leu His Leu His Gly Thr Gly Ile Gln
 980 985 990

Val

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 994 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

B
 Met Val Val Gln Thr Arg Phe Pro Ser Trp Ile Ile Leu Cys Tyr Ile
 1 5 10 15
 Trp Leu Leu Gly Phe Ala His Thr Gly Glu Ala Gln Ala Ala Lys Glu
 20 25 30
 Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile
 35 40 45
 Ser Ser Pro Pro Ser Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn
 50 55 60
 Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn
 65 70 75 80
 Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln
 85 90 95
 Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu
 100 105 110
 Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr
 115 120 125
 Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val
 130 135 140
 Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu
 145 150 155 160
 Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro
 165 170 175
 Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys
 180 185 190
 Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Thr Ile
 195 200 205

Val Glu Asn Leu Ala Val Phe Pro Asp Thr Val Thr Gly Ser Glu Phe
 210 215 220

Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu
 225 230 235 240

Glu Ala Glu Asn Ser Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp
 245 250 255

Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys
 260 265 270

Gly Asp Thr Cys Glu Pro Cys Gly Arg Arg Phe Tyr Lys Ser Ser Ser
 275 280 285

Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Arg
 290 295 300

Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro
 305 310 315 320

Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln
 325 330 335

Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser
 340 345 350

Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu
 355 360 365

Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser
 370 375 380

Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val
 385 390 395 400

Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu
 405 410 415

Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala
 420 425 430

Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly
 435 440 445

Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Gln Leu Ser Trp Gln
 450 455 460

Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr
 465 470 475 480

Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Leu Lys Thr Lys
 485 490 495

Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val
 500 505 510

Phe Gln Ile Arg Ala Val Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro
 515 520 525

Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Ser Gly Lys Met Phe Glu
 530 535 540

Ala Thr Ala Val Ser Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val
 545 550 555 560

Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe
 565 570 575

Ile Ile Gly Arg Arg His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly
 580 585 590

Asp Glu Glu Leu Tyr Phe His Cys Thr Lys Thr Tyr Ile Asp Pro Glu
 595 600 605

Thr Tyr Glu Asp Pro Asn Arg Ala Val His Gln Phe Ala Lys Glu Leu
 610 615 620

Asp Ala Ser Cys Ile Lys Ile Glu Arg Val Ile Gly Ala Gly Glu Phe
 625 630 635 640

Gly Glu Val Cys Ser Gly Arg Leu Lys Leu Pro Gly Gln Arg Asp Val
 645 650 655

Ala Val Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr Glu Lys Gln Arg
 660 665 670

Arg Asp Phe Leu Cys Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro
 675 680 685

Asn Val Val His Leu Glu Gly Val Val Thr Arg Gly Lys Pro Val Met
 690 695 700

Ile Val Ile Glu Phe Met Glu Asn Gly Ala Leu Asp Ala Phe Leu Arg
 705 710 715 720

Lys His Asp Gly Gln Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg
 725 730 735

Gly Ile Ala Ala Gly Met Arg Tyr Leu Ala Asp Met Gly Tyr Val His
 740 745 750

Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys
 755 760 765

Lys Val Ser Asp Phe Gly Leu Ser Arg Val Ile Glu Asp Asp Pro Glu
 770 775 780

Ala Val Tyr Thr Thr Thr Gly Gly Lys Ile Pro Val Arg Trp Thr Ala
 785 790 795 800
 Pro Glu Ala Ile Gln Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp
 805 810 815
 Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr Gly Glu Arg Pro
 820 825 830
 Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala Ile Glu Glu Gly
 835 840 845
 Tyr Arg Leu Pro Ala Pro Met Asp Cys Pro Ala Gly Leu His Gln Leu
 850 855 860
 Met Leu Asp Cys Trp Gln Lys Asp Arg Ala Glu Arg Pro Lys Phe Glu
 865 870 875 880
 Gln Ile Val Gly Ile Leu Asp Lys Met Ile Arg Asn Pro Ser Ser Leu
 885 890 895
 Lys Thr Pro Leu Gly Thr Cys Ser Arg Pro Leu Ser Pro Leu Leu Asp
 900 905 910
 Gln Ser Thr Pro Asp Phe Thr Ala Phe Cys Ser Val Gly Glu Trp Leu
 915 920 925
 Gln Ala Ile Lys Met Glu Arg Tyr Lys Asp Asn Phe Thr Ala Ala Gly
 930 935 940
 Tyr Asn Ser Leu Glu Ser Val Ala Arg Met Thr Ile Asp Asp Val Met
 945 950 955 960
 Ser Leu Gly Ile Thr Leu Val Gly His Gln Lys Lys Ile Met Ser Ser
 965 970 975
 Ile Gln Thr Met Arg Ala Gln Met Leu His Leu His Gly Thr Gly Ile
 980 985 990
 Gln Val